1. (Currently Amended) A method for at least one of genotyping or ~~and~~ haplotyping a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample, comprising:

i) providing one or more microarrays that include a set of oligonucleotide probes that are capable of detecting the at least one of the genotypes, ~~and~~ the haplotypes or the strain variant;

ii) hybridizing the DNA sample to the one or more microarrays to create a hybridization pattern; ~~and~~

iii) determining at least one of a genotype, ~~and~~ a haplotype or a strain variant based on the hybridization pattern; and

iv) optimizing at least one of the set or an arrangement of the oligonucleotide probes as a function of at least one of a match criteria or a mismatch criteria between a true allele contained in the DNA sample and an allele determined by the hybridizing step.

2. (Withdrawn) The method of claim 1, wherein the one or more microarrays include a set of oligonucleotide probes that are capable of detecting at least one of all known genotypes or all known haplotypes at the polymorphic genetic loci or the strain identification.

3. (Currently Amended) The method of claim 1, wherein the one or more microarrays are configured to include at least one of an optimal set or ~~and~~ an optimal arrangement of oligonucleotide probes.

Claim 4 (Cancelled).

5. (Previously Presented) The method of claim 81, wherein the weights are provided as follows: $w_j = 1 \forall_j$, wherein $\forall_j$ is a set of at least one of all known genotypes or all known haplotypes at one or more predetermined polymorphic genetic loci.

6. (Previously Presented) The method of claim 81, wherein the weights are provided as follows: w_j is different for each genotype or haplotype.

7. (Currently Amended) ~~The method of claim 1~~A method for at least one of genotyping or haplotyping a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample, comprising:

i) providing one or more microarrays that include a set of oligonucleotide probes that are capable of detecting the at least one of the genotypes, the haplotypes or the strain variant;

ii) hybridizing the DNA sample to the one or more microarrays to create a hybridization pattern; and

iii) determining at least one of a genotype, a haplotype or a strain variant based on the hybridization pattern,

wherein step (iii) produces a vector of *n* measurements, and wherein *n* is a number of probes contained on the one or more microarrays.

8. (Original) The method of claim 7, wherein the *n* potential probes provided to identify *N* known genotypes or haplotypes are each associated with a response vector $\vec{v}_j \in \{0,1\}^N, j = 1,...,n.$

9. (Original) The method of claim 8, further comprising generating a graph *G* on vertices corresponding to probe response vectors.

10. (Original) The method of claim 9, wherein the graph *G* is a complete edge-weighted and vertex-weighted undirected graph *G* = (*V*, *E*) provided on *n* vertices, wherein *n* is the number of potential probes.

11. (Original) The method of claim 10, wherein the weights *w* of each vertex *v* and each edge *e* are constrained by: $0 \le w(v), w(e) \le 1$.

12. (Original) The method of claim 11, wherein the weight *w* of a vertex *v* is set to:

w(*v*) = min{fraction of 0's, fraction of 1's}.

13. (Previously Presented) The method of claim 11, wherein the weight *w* of an edge *e* ={*u*,*v*} is set to:

w(e) = Hamming distance/vector length,

wherein Hamming distance is measured between the probe response vectors corresponding to vertices *u* and *v*, and vector length is the length of the probe response vectors, namely, *N*.

14. (Original) The method of claim 10, further comprising modifying the graph G by thresholding the edges such that the modified graph G_{mod} is defined as $G_{mod} = (V, E_{mod})$, wherein $E_{mod} = \{e \in E: w(e) \leq \rho\}$, and ρ is a selected threshold value.

15. (Currently Amended) The method of claim 14, wherein, for the modified graph G_{mod} and the probe set size M, the following is performed:

i) initializing a current-best list of independent sets with associated information weights,

ii) initializing vertex boosting weights to vertex weights $w(v)$,

iii) defining a probability distribution on the vertex subset based on vertex boosting weights,

iv) choosing a random subset of vertices of a specified size M based on the probability distribution,

v) eliminating one of the end-point vertices in each of the edges remaining in the induced subgraph on the random subset,

vi) modifying the vertex boosting weights by increasing the weights of the vertices that are retained in the subset and decreasing the weights of the vertices that were selected in step (iv) but eliminated in step (v), and

vii) repeating steps (iii) through (vi) for at least one of a predetermined number of iterations or ~~and~~ until no improvement to the list of top independent sets is achieved.

16. (Original) The method of claim 15, wherein, for the modified graph G_{mod} and the probe set size M, steps (ii) through (vii) are repeated for a predetermined number of iterations, each iteration starting with reinitializing vertex boosting weights to vertex weights $w(v)$ in step (ii).

17. (Original) The method of claim 16, wherein, for a given fixed small $0<\epsilon<<1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq 1) > 1-\epsilon$.

18. (Original) The method of claim 16, wherein, for a given fixed small $0<\epsilon<<1$ and a fixed $\alpha>1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq \alpha) > 1-\epsilon$.

19. (Original) The method of claim 15, wherein the threshold ρ has a value to enable the graph G to have a sparsity bounded by $A \leq$ sparsity $\leq B$, wherein the sparsity is definable by the average degree of a vertex in the graph G.

20. (Original) The method of claim 19, wherein the lower bound A is a relatively small constant, and the upper bound B is a function of the number of vertices n.

Claims 21-40 (Cancelled).

41. (Currently Amended) A non-transitory storage medium which includes thereon a software arrangement for providing one or more microarrays, which ~~is capable of~~ configure~~sing~~ a processing arrangement to perform the ~~steps~~ procedures comprising:

i) receiving information regarding a hybridization of the DNA sample to one or more microarrays to create a hybridization pattern, the one or more microarrays including a set of oligonucleotide probes that are capable of detecting at least one set of genotypes or ~~and~~ haplotypes for a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample; ~~and~~

ii) determining at least one of a genotype, ~~and~~ a haplotype or a strain variant based on the hybridization pattern; and

iii) optimizing at least one of the set or an arrangement of the oligonucleotide probes as a function of at least one of a match criteria or a mismatch criteria between a true allele contained in the DNA sample and an allele determined from the hybridization.

Claims 42-60 (Cancelled).

61. (Currently Amended) A system for at least one of genotyping or ~~and~~ haplotyping polymorphic genetic loci or strain identification in a deoxyribonucleic acid (DNA) sample, comprising:

a processing device ~~arrangement which is capable of being programmed~~ which, when executed, is configured to:

i) receive information regarding a hybridization of the DNA sample to one or more microarrays to create a hybridization pattern, the one or more microarrays including a set of oligonucleotide probes that are capable of

detecting at least one set of genotypes or ~~and~~ haplotypes for a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample; ~~and~~

ii) determine at least one of a genotype, ~~and~~ a haplotype or a strain variant based on the hybridization pattern; and

iii) optimize at least one of the set or an arrangement of the oligonucleotide probes as a function of at least one of a match criteria or a mismatch criteria between a true allele contained in the DNA sample and an allele determined by the hybridization.

Claims 62-80 (Cancelled).

81. (Currently Amended) The method of ~~according to~~ claim 1-4, wherein the mismatch criteria is the following:

$$\min \sum_{\text{type } j} w_j \; E\left[\Pi_{T_j \neq \hat{T}_j}\right]$$
$$\Leftrightarrow \quad \min \sum_{\text{type } j} w_j \; \Pr\left(T_j \neq \hat{T}_j\right).$$

wherein T_j is a true allele contained in the DNA sample, $\hat{T}_j$ is the allele determined by the hybridization step, $\Pi_x = \begin{Bmatrix} 1, & \text{if } X \text{ is true} \\ 0, & \text{otherwise} \end{Bmatrix}$, and w_j is a weight assigned to at least one of the genotype ~~and~~ or the haplotype j.

82. (New) The method of claim 1, further comprising: at least one of displaying or storing data associated with the at least one of the genotype, the haplotype or the strain

variant in a storage arrangement in at least one of a user-accessible format or a user-readable format.

83. (New) The method of claim 7, further comprising: at least one of displaying or storing data associated with at least one of the genotype, the haplotype, the strain variant or the vector in a storage arrangement in at least one of a user-accessible format or a user-readable format.

84. (New) The storage medium of claim 41, wherein the mismatch criteria is the following:

$$\min \sum_{type\ j} w_j \; E\left[\Pi_{T_j \neq \hat{T}_j}\right]$$
$$\Leftrightarrow \quad \min \sum_{type\ j} w_j \; \Pr\left(T_j \neq \hat{T}_j\right).$$

wherein T_j is a true allele contained in the DNA sample, $\hat{T}_j$ is the allele determined by the hybridization step, $\Pi_X = \begin{Bmatrix} 1, & \text{if } X \text{ is true} \\ 0, & \text{otherwise} \end{Bmatrix}$, and w_j is a weight assigned to at least one of the genotype or the haplotype *j*.

85. (New) The storage medium of claim 84, wherein the weights are provided as follows: $w_j = 1 \; \forall_j$, wherein $\forall_j$ is a set of at least one of all known genotypes or all known haplotypes at one or more predetermined polymorphic genetic loci.

86. (New) The storage medium of claim 84, wherein the weights are provided as follows: w_j is different for each genotype or haplotype.

87. (New) The system of claim 61, wherein the mismatch criteria is the following:

$$\min \sum_{type\ j} w_j \ E\left[\Pi_{T_j \neq \hat{T}_j}\right]$$
$$\Leftrightarrow \ \min \sum_{type\ j} w_j \ \Pr\left(T_j \neq \hat{T}_j\right).$$

wherein T_j is a true allele contained in the DNA sample, $\hat{T}_j$ is the allele determined by the hybridization step, $\Pi_X = \begin{Bmatrix} 1, & \text{if } X \text{ is true} \\ 0, & \text{otherwise} \end{Bmatrix}$, and w_j is a weight assigned to at least one of the genotype or the haplotype *j*.

88. (New) The system of claim 87, wherein the weights are provided as follows: $w_j = 1 \forall_j$, wherein $\forall_j$ is a set of at least one of all known genotypes or all known haplotypes at one or more predetermined polymorphic genetic loci.

89. (New) The system of claim 87, wherein the weights are provided as follows: w_j is different for each genotype or haplotype.

90. (New) A non-transitory computer-accessible medium having stored thereon computer executable instructions for at least one of genotyping or haplotyping a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample, wherein, when the executable

instructions are executed by a processing arrangement, configure the processing arrangement to:

i) provide one or more microarrays that include a set of oligonucleotide probes that are capable of detecting the at least one of the genotypes, the haplotypes or the strain variant;

ii) hybridize the DNA sample to the one or more microarrays to create a hybridization pattern; and

iii) determine at least one of a genotype, a haplotype or a strain variant based on the hybridization pattern,

wherein procedure (iii) produces a vector of *n* measurements, and wherein *n* is a number of probes contained on the one or more microarrays.

91. (New) The computer-accessible medium of claim 90, wherein the *n* potential probes provided to identify *N* known genotypes or haplotypes are each associated with a response vector $\vec{v}_j \in \{0,1\}_j^N, j=1,...,n.$

92. (New) The computer-accessible medium of claim 91, further comprising generating a graph *G* on vertices corresponding to probe response vectors, wherein the graph *G* is a complete edge-weighted and vertex-weighted undirected graph *G* = (*V*, *E*) provided on *n* vertices, wherein *n* is the number of potential probes.

93. (New) The computer-accessible medium of claim 92, wherein the weights *w* of each vertex *v* and each edge *e* are constrained by: $0 \le w(v), w(e) \le 1$.

94. (New) The computer-accessible medium of claim 93, wherein at least one of (i) the weight w of a vertex v is set to: $w(v)$ = min{fraction of 0's, fraction of 1's}, or (ii) the weight w of an edge $e = \{u,v\}$ is set to: $w(e)$ = Hamming distance/vector length, wherein the Hamming distance is measured between the probe response vectors corresponding to vertices u and v, and wherein the vector length is the length of the probe response vectors N.

95. (New) The computer-accessible medium of claim 92, further comprising modifying the graph G by thresholding the edges such that the modified graph G_{mod} is defined as $G_{mod} = (V, E_{mod})$, wherein $E_{mod} = \{e \in E: w(e) \leq \rho\}$, and ρ is a selected threshold value.

96. (New) The computer-accessible medium of claim 95, wherein, for the modified graph G_{mod} and the probe set size M, when the executable instructions are executed, the processing arrangement is further configured to:

iv) initialize a current-best list of independent sets with associated information weights,

v) initialize vertex boosting weights to vertex weights $w(v)$,

vi) defining a probability distribution on the vertex subset based on vertex boosting weights,

vii) choose a random subset of vertices of a specified size M based on the probability distribution,

viii) eliminate one of the end-point vertices in each of the edges remaining in the induced subgraph on the random subset,

ix) modify the vertex boosting weights by increasing the weights of the vertices that are retained in the subset and decreasing the weights of the vertices that were selected in procedure (vii) but eliminated in procedure (viii), and

x) repeat procedures (vi) through (ix) for at least one of a predetermined number of iterations or until no improvement to the list of top independent sets is achieved.

97. (New) The computer-accessible medium of claim 96, wherein, for the modified graph G_{mod} and the probe set size M, when executed, the processing arrangement is further configured to repeat procedures (v) through (x) for a predetermined number of iterations, and to start each iteration with a reinitialization of the vertex boosting weights to the vertex weights $w(v)$ in procedure (v).

98. (New) The computer-accessible medium of claim 97, wherein at least one of (i) for a given fixed small $0<\epsilon<<1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq 1) > 1-\epsilon$, or (ii) for a given fixed small $0<\epsilon<<1$ and a fixed $\alpha>1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq \alpha) > 1-\epsilon$.

99. (New) The computer-accessible medium of claim 96, wherein the threshold ρ has a value to enable the graph G to have a sparsity bounded by $A \leq$ sparsity $\leq B$, wherein the sparsity is definable by the average degree of a vertex in the graph G, wherein the

lower bound A is a relatively small constant, and wherein the upper bound B is a function of the number of vertices n.

100. (New) A system for at least one of genotyping or haplotyping a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample, comprising:

a processing device that, when executed, is configured to:

i) provide one or more microarrays that include a set of oligonucleotide probes that are capable of detecting the at least one of the genotypes, the haplotypes or the strain variant;

ii) hybridize the DNA sample to the one or more microarrays to create a hybridization pattern; and

iii) determine at least one of a genotype, a haplotype or a strain variant based on the hybridization pattern,

wherein procedure (iii) produces a vector of n measurements, and wherein n is a number of probes contained on the one or more microarrays.

101. (New) The system of claim 100, wherein the n potential probes provided to identify N known genotypes or haplotypes are each associated with a response vector $\vec{v}_j \in \{0,1\}^N, j = 1,...,n.$

102. (New) The system of claim 101, further comprising generating a graph G on vertices corresponding to probe response vectors, wherein the graph G is a complete

edge-weighted and vertex-weighted undirected graph $G = (V, E)$ provided on n vertices, wherein n is the number of potential probes.

103. (New) The system of claim 102, wherein the weights w of each vertex v and each edge e are constrained by: $0 \leq w(v), w(e) \leq 1$.

104. (New) The system of claim 103, wherein at least one of (i) the weight w of a vertex v is set to: $w(v)$ = min{fraction of 0's, fraction of 1's}, or (ii) the weight w of an edge e ={u,v} is set to: $w(e)$ = Hamming distance/vector length, wherein the Hamming distance is measured between the probe response vectors corresponding to vertices u and v, and wherein the vector length is the length of the probe response vectors N.

105. (New) The system of claim 102, further comprising modifying the graph G by thresholding the edges such that the modified graph G_{mod} is defined as $G_{mod} = (V, E_{mod})$, wherein $E_{mod} = \{e \in E: w(e) \leq \rho\}$, and ρ is a selected threshold value.

106. (New) The system of claim 105, wherein, for the modified graph G_{mod} and the probe set size M, when executed, the processing device is further configured to:

iv) initialize a current-best list of independent sets with associated information weights,

v) initialize vertex boosting weights to vertex weights $w(v)$,

vi) define a probability distribution on the vertex subset based on vertex boosting weights,

vii) choose a random subset of vertices of a specified size *M* based on the probability distribution,

viii) eliminate one of the end-point vertices in each of the edges remaining in the induced subgraph on the random subset,

ix) modify the vertex boosting weights by increasing the weights of the vertices that are retained in the subset and decreasing the weights of the vertices that were selected in procedure (vii) but eliminated in procedure (viii), and

x) repeat procedures (vi) through (ix) for at least one of a predetermined number of iterations or until no improvement to the list of top independent sets is achieved.

107. (New) The system of claim 106, wherein, for the modified graph G_{mod} and the probe set size *M*, when executed, the processing device is further configured to repeat procedures (v) through (x) for a predetermined number of iterations, and to start each iteration with a reinitialization of the vertex boosting weights to the vertex weights $w(v)$ in procedure (v).

108. (New) The computer-accessible medium of claim 107, wherein at least one of (i) for a given fixed small $0<\epsilon<<1$, the probe set size *M* satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq 1) > 1-\epsilon$, or (ii) for a given fixed small $0<\epsilon<<1$ and a fixed $\alpha>1$, the probe set size *M* satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq \alpha) > 1-\epsilon$.

109. (New) The computer-accessible medium of claim 106, wherein the threshold ρ has a value to enable the graph G to have a sparsity bounded by $A \leq$ sparsity $\leq B$, wherein the sparsity is definable by the average degree of a vertex in the graph G, wherein the lower bound A is a relatively small constant, and wherein the upper bound B is a function of the number of vertices n.